IV. AMENDMENTS TO THE CLAIMS

1-8. (Canceled)

9. (Currently Amended) A process for the ~~fermentative of~~ production of an L-amino acid~~, in particular lysine, which comprises carrying out the following steps~~ comprising:

a) ~~fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the sigE gene or nucleotide sequence which code for it are enhanced, in particular overexpressed~~ culturing a coryneform bacterium under conditions suitable for overexpression of the sigE gene having the nucleic acid sequence as set forth in SEQ ID NO: 1 and encoding a polypeptide having an amino acid sequence as set forth in SEQ ID NO: 2;

b) ~~concentration of L-amino acid in the medium or in the cells of the bacteria, and~~ enriching the medium or the cells of the bacterium;

c) ~~isolation of the~~ isolating the L-amino acid.

10. (Canceled)

11. (Canceled)

12. (Currently Amended) A process ~~as claimed in~~ according to claim 9, wherein ~~a strain~~ said bacteria have been transformed with a plasmid vector ~~is employed, and the plasmid vector carries the nucleotide sequence which codes for the sigE gene~~ which comprises the nucleotide sequence of SEQ ID NO: 1.

13. (Currently Amended) A process as claimed in claim 9, wherein ~~the expression of the polynucleotide(s) which code(s) for the sigE gene is enhanced, in particular over-expressed~~ said overexpression is achieved by increasing the copy number of the sigE gene.

14. (Canceled)

15. (Currently Amended) ~~A~~ The process ~~as claimed in~~ according to claim 9, ~~wherein the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of~~ wherein in a *C. glutamicum* strain, one or more of the genes selected from the group is overexpressed:

~~15.1~~ (a) the dapA gene which codes for dihydrodipicolinate synthase,

~~15.2~~ (b) the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

~~15.3~~ (c) the tpi gene which codes for triose phosphate isomerase,

~~15.4~~ (d) the pgk gene which codes for 3-phosphoglycerate kinase,

~~15.5~~ (e) the zwf gene which codes for glucose 6-phosphate dehydrogenase,

~~15.6~~ (f) the pyc gene which codes for pyruvate carboxylase,

~~15.7~~ (g) the mqo gene which codes for malate-quinone oxidoreductase,

~~15.8~~ (h) the lysC gene which codes for ~~feed-back-resistant~~ aspartate kinase,

~~15.9~~ (i) the lysE gene ~~which codes~~ coding for a protein for lysine export,

~~15.10~~ (j) the hom gene which codes for homoserine dehydrogenase,

~~15.11~~ (j) the ilvA gene which codes for threonine dehydratase ~~or the ilvA(Fbr) allele which codes for a feed-back-resistant threonine dehydratase~~,

~~15.12~~ (k) the ilvBN gene which codes for acetohydroxy-acid synthase,

~~15.13~~ (l) the ilvD gene which codes for dihydroxy-acid dehydratase, and

~~15.14~~ (m) the zwa1 gene which codes for the Zwa1 protein.

~~is or are enhanced or over-expressed are fermented.~~

16. (Currently Amended) A process as claimed in claim 9, wherein ~~for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of~~ in a *C. glutamicum* strain, one or more of the genes selected from the following group is deleted:

~~16.1~~ (a) the pck gene which codes for phosphoenol pyruvate carboxykinase,

~~16.2~~ (b) the pgi gene which codes for glucose 6-phosphate isomerase,

~~16.3~~ (c) the poxB gene which codes for pyruvate oxidase, and

~~16.4~~ (d) the zwa2 gene which codes for the Zwa2 protein.

~~is or are attenuated are fermented.~~

17. (Canceled)

18. (Currently Amended) A process ~~as claimed in one or more of the preceding claims, wherein microorganisms of the genus Corynebacterium are employed~~ according to claim 9, wherein said coryneform bacteria are of the species *Corynebacterium glutamicum*.

19. (Canceled)

20. (Canceled)

21. (New) The process according to claim 9, wherein said L-amino acid is L-lysine.

22. (New) The process according to claim 9, wherein said nucleotide sequence comprises nucleotides 302 to 949 of SEQ ID NO: 1.

23. (New) A process for producing L-amino acids comprising:

a) transforming a coryneform bacterium with a vector which includes a sigE gene having the polynucleotide sequence of SEQ ID NO: 1, wherein said sigE gene is under control of a promoter which allows the overexpression of said sigE gene;

b) culturing said bacterium in a medium suitable for expression of the sigE gene to thereby produce L-amino acids; and

c) isolating the L-amino acids.

24. (New) A method for the preparation of L-amino acids, comprising:

culturing coryneform bacteria, which include an overexpressed sigE gene having a polynucleotide sequence which encodes the amino acid sequence of SEQ ID NO: 2, in a medium suitable for the expression of sigE to thereby produce L-amino acids.

25. (New) The method according to claim 24, further comprising isolating the L-amino acids.

26. (New) The method according to claim 24, wherein the bacteria have been transformed with a plasmid vector which comprises the nucleotide sequence of SEQ ID NO: 1.

27. (New) The method according to claim 24, wherein the coryneform bacteria bacteria produce L-lysine.

28. (New) A method according to claim 24, wherein the bacteria are *Corynebacterium glutamicum*.